

What is claimed is:

1. A method of identifying an animal which possesses a genotype indicative of the metabolic traits of fat content, growth rate, and feed consumption, the method comprising:

- a) obtaining a nucleic acid sample from the animal, and
- b) identifying a polymorphism in the MC4R gene of the sample.

2. The method of claim 1 wherein the polymorphism is characterized by a nucleotide position 678 of the PCR product of the MC4R gene.

3. The method of claim 1 wherein the animal is a pig.

4. The method of claim 2 wherein the polymorphism at the nucleotide position 678 is associated with fat content.

5. The method of claim 2 wherein a guanine at the nucleotide position 678 is associated with lower feed intake.

6. The method of claim 2 wherein an adenine at the nucleotide position 678 is associated with a faster rate of gain.

7. The method of claim 1 wherein the step of identifying the polymorphism is a method employing allele specific oligonucleotides.

8. The method of claim 1 wherein the step of identifying the polymorphism is selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), temperature gradient gel electrophoresis (TGGE), and use of linked genetic markers.

9. The method of claim 8 wherein the step of identifying the polymorphism comprises RFLP analysis.

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10. The method of claim 1 further comprising the step of amplifying the MC4R gene sequence.

5 11. The method of claim 10 further comprising the step of digesting the amplified region with the restriction endonuclease *Taq I*.

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10 12. The amplified gene sequence of claim 10 wherein primers used in the amplification are selected from the group consisting of SEQ. ID NO:6, SEQ. ID NO:7, SEQ. ID NO:8, SEQ. ID NO:9, SEQ. ID NO:10, and SEQ. ID NO:11.

13. A single strand of an oligonucleotide primer useful for detecting nucleotide 678 of the PCR product of a MC4R gene the primer consisting of a nucleotide sequence having about 4-30 contiguous bases from SEQ ID NO:1.

15 14. The oligonucleotide of claim 13 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:6.

20 15. The oligonucleotide of claim 13 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:7.

16. The oligonucleotide of claim 13 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:8.

25 17. The oligonucleotide of claim 13 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:9.

18. The oligonucleotide of claim 13 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:10.

30 19. The oligonucleotide of claim 13 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:11.

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20. A method of identifying an animal which possess a desired genotype indicative of the metabolic traits of fat content, growth rate, and feed consumption, the method comprising

- a) obtaining a sample of genomic DNA,
- b) digesting the sample with *Taq I* to obtain fragments,
- c) separating the fragments obtained from the digestion, and
- d) identifying the presence or absence of a *Taq I* site at base 678 of the PCR product of the MC4R gene.

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21. The method of claim 20 further comprising the step of selecting animals with the desired genotype for breeding.

22. The method of claim 20 wherein the site is identifiable by fragments of 466, 225, and 76 bp when a guanine is present at base 678 and fragments of 542 and 225 bp when an adenine is present when a restriction enzyme which cuts at the same recognition site as *Taq I* is used.

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23. The method of claim 20 wherein the step of identifying comprises detecting the *Taq I* site by amplification.

24. A kit for evaluating a sample of animal DNA comprising a reagent in a container that identifies a polymorphism in a MC4R gene.

25. The kit of claim 24 wherein the reagent is a primer that amplifies the MC4R gene or a fragment thereof.

26. The kit of claim 24 further comprising a DNA polymerase which cleaves the MC4R gene, a forward primer, and a reverse primer, wherein the primers are capable of amplifying a region of the MC4R gene which contains a polymorphic site.

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27. A primer for assaying the presence of a polymorphic *TaqI* site in the MC4R gene wherein the primer comprises a sequence selected from the group consisting of SEQ. ID NO:6, SEQ. ID NO:7, SEQ. ID NO:8, SEQ. ID NO:9, SEQ. ID NO:10, and SEQ. ID NO:11.

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28. A method for selecting animals for the desired traits of lower fat content, faster growth rate, or lower feed consumption comprising the steps of

- obtaining a nucleic acid sample from an animal,
- identifying a polymorphism characterized by a nucleotide position 678 of a PCR product of the MC4R gene, and
- selecting the animals which have the nucleotide associated with the desired traits in position 678.

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29. A method for an indirect selection for a polymorphism in MC4R wherein specific alleles of an alternative DNA marker are used to make the indirect selection wherein the alternative DNA marker is a linked marker near MC4R.

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30. The method of claim 29 wherein the linked marker is selected from the group consisting of S0331, BHT0433, and S0313.

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31. A method of identifying animals which possess a desired genotype indicative of the metabolic traits of fat content, growth rate, and feed consumption, the method comprising

- determining an association between a MC4R genotype and a trait of interest by obtaining a sample of animals from a line or breed of interest,
- preparing genomic DNA from each animal in the sample,
- determining the genotype of the MC4R gene, and
- calculating the association between the MC4R genotype and the trait.

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32. A method of selecting animals which possess a desired MC4R genotype indicative of the metabolic traits of fat content, growth rate, and feed consumption, the method comprising

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- obtaining a nucleic acid sample from an animal,

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- b) identifying the genotype of the MC4R gene of the animal, and
- c) selecting those animals which have the genotype associated with the desired traits.

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